

# SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Nucleotide sequences which code for the methH gene

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (385)..(4047)

<223> methH gene

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tgtccacgat gtgctttgcg atgtgggtgt gaggccaaga ggtggctttt acgtcgtcaa 180

gcaatttttag ccactcttcc cacggctttc cggtgccgtt gaggatagct tcaggggaca 240

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tgccctggtgt tgagccttgc ggagtggagt cagtcatgcy accgagacta gtggcgcttt 300

gcctgtgttg cttaggcggc gttgaaaatg aactacgaat gaaaagtctg ggaattgtct 360

aatccgtact aagctgtcta caca atg tct act tca gtt act tca cca gcc 411

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Met Ser Thr Ser Val Thr Ser Pro Ala

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cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg ttg gca aac cat 459

His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala Leu Ala Asn His

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gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc caa ggc ttt gac 507

Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu Gln Gly Phe Asp

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ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg tgt aat gag att 555

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ctc aac gac acc cgc cct gat gtg ttg agg cag att cac cgc gcc tac 603

Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile His Arg Ala Tyr

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ttt gag gcg gga gct gac ttg gtt gag acc aat act ttt ggt tgc aac 651

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25	tgt gtg gat att gcc aag cag caa acc cgc gat ggt gca cac atg ctg Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly Ala His Met Leu 395 400 405			1611
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40	gac tcc acc gag cca gag gtt att cgc aca ggc ctt gag cac ttg ggt Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu Glu His Leu Gly 445 450 455			1755
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50	gag tcc cgc tac cag cgc atc atg aaa ctg gta aag cag cac ggt gcg Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys Gln His Gly Ala 475 480 485			1851
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60	gag cac aag gtg cgc att gct aaa cga ctg att gac gat atc acc ggc Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp Asp Ile Thr Gly 510 515 520			1947
65	agc tac ggc ctg gat atc aaa gac atc gtt gtg gac tgc ctg acc ttc Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp Cys Leu Thr Phe 525 530 535			1995



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	830 835 840	
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	875 880 885	
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<212> PRT

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Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe  
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Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu  
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Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr  
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Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val  
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Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg  
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Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu  
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Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala  
180 185 190

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Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu  
210 215 220

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10	Arg Asn Glu Arg Ser Arg Lys Ile Ala Ala Glu Arg Lys Ala Asn Ala	915	920	925	
	Ala Pro Val Ile Val Pro Glu Arg Ser Asp Val Ser Thr Asp Thr Pro	930	935	940	
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20	Leu Ala Glu Phe Leu Gly Asn Leu Asp Glu Arg Ala Leu Phe Met Gly	965	970	975	
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25	Asp Leu Val Glu Thr Glu Gly Arg Pro Arg Leu Arg Tyr Trp Leu Asp	995	1000	1005	
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35	Gln Arg Gly Arg Phe Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu	1060	1065	1070	
40	Gln Ala Val Lys Asp Gly Gln Val Asp Val Met Pro Phe Gln Leu Val	1075	1080	1085	
	Thr Met Gly Asn Pro Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala	1090	1095	1100	
45	Asn Glu Tyr Arg Glu Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu	1105	1110	1115	1120
	Thr Glu Ala Leu Ala Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu	1125	1130	1135	
50	Lys Leu Asn Asp Gly Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys	1140	1145	1150	
	Thr Lys Phe Phe Asp Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly	1155	1160	1165	
55	Tyr Gly Ser Cys Pro Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu	1170	1175	1180	
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Leu Glu Pro Gly Arg Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu  
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